647

OIPE

ENTERED #8

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/903,323A

DATE: 03/18/2002
TIME: 15:36:32

Input Set : A:\510015-261.TXT
Output Set: N:\CRF3\03182002\I903323A.raw

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4  <110> APPLICANT: De Robertis, Edward M.
5          Bouwmeester, Tewis
8  <120> TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
9          Factors
11 <130> FILE REFERENCE: 510015-261
13 <140> CURRENT APPLICATION NUMBER: US 09/903,323A
14 <141> CURRENT FILING DATE: 2001-07-11
16 <150> PRIOR APPLICATION NUMBER: US 60/020,150
17 <151> PRIOR FILING DATE: 1996-06-20
19 <160> NUMBER OF SEQ ID NOS: 10
21 <170> SOFTWARE: FastSEQ for Windows Version 3.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 270
25 <212> TYPE: PRT
26 <213> ORGANISM: Xenopus
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32              20                  25                  30
33 Ser Leu Asn Ser Arg Gly Tyr Phe Arg Lys Glu Arg Gly Ala Arg Arg
34          35                  40                  45
35 Ser Lys Ile Leu Leu Val Asn Thr Lys Gly Leu Asp Glu Pro His Ile
36      50                  55                  60
37 Gly His Gly Asp Phe Gly Leu Val Ala Glu Leu Phe Asp Ser Thr Arg
38  65                  70                  75                  80
39 Thr His Thr Asn Arg Lys Glu Pro Asp Met Asn Lys Val Lys Leu Phe
40                  85                  90                  95
41 Ser Thr Val Ala His Gly Asn Lys Ser Ala Arg Arg Lys Ala Tyr Asn
42              100                 105                 110
43 Gly Ser Arg Arg Asn Ile Phe Ser Arg Arg Ser Phe Asp Lys Arg Asn
44              115                 120                 125
45 Thr Glu Val Thr Glu Lys Pro Gly Ala Lys Met Phe Trp Asn Asn Phe
46          130                 135                 140
47 Leu Val Lys Met Asn Gly Ala Pro Gln Asn Thr Ser His Gly Ser Lys
48  145                 150                 155                 160
49 Ala Gln Glu Ile Met Lys Glu Ala Cys Lys Thr Leu Pro Phe Thr Gln
50                  165                 170                 175
51 Asn Ile Val His Glu Asn Cys Asp Arg Met Val Ile Gln Asn Asn Leu
52              180                 185                 190
53 Cys Phe Gly Lys Cys Ile Ser Leu His Val Pro Asn Gln Gln Asp Arg
54              195                 200                 205
55 Arg Asn Thr Cys Ser His Cys Leu Pro Ser Lys Phe Thr Leu Asn His
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56        210                215                220
57   Leu Thr Leu Asn Cys Thr Gly Ser Lys Asn Val Val Lys Val Val Met
58   225                230                235                240
59   Met Val Glu Glu Cys Thr Cys Glu Ala His Lys Ser Asn Phe His Gln
60        .          245                250                255
61   Thr Ala Gln Phe Asn Met Asp Thr Ser Thr Thr Leu His His
62                  260                265                270
64   <210> SEQ ID NO: 2
65   <211> LENGTH: 1338
66   <212> TYPE: DNA
67   <213> ORGANISM: Xenopus
69   <400> SEQUENCE: 2
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71   atgtactcag gatctgtatt atcgtctgcc ttgtgaatga tggagcagga aaacactcag      120
72   aaggacgaga aaggacaaaa acatattcac ttaacagcag aggttacttc agaaaagaaa      180
73   gaggagcacg taggagcaag attctgctgg tgaatactaa aggtcttgat gaaccccaca      240
74   ttgggcatgg tgattttcgc ttagtagctg aactatttga ttccaccaga acacatacaa      300
75   acagaaaaga gccagacatg aacaaagtca agcttttctc aacagttgcc catggaaaca      360
76   aaagtgcaag aagaaaagct tacaatggtt ctagaaggaa tatttttcct cgccgttctt      420
77   ttgataaaag aaatacagag gttactgaaa agcctggtgc caagatgttc tggaacaatt      480
78   ttttggttaa aatgaatgga gccccacaga atacaagcca tggcagtaaa gcacaggaaa      540
79   taatgaaaga agcttgcaaa accttgtttt tcactcagaa tattgtacat gaaaactgtg      600
80   acaggatggt gatacagaac aatctgtgct ttggtaaatg catctctctc catgttccaa      660
81   atcagcaaga tcgacgaaat acttgttccc attgcttgcc gtccaaattt accctgaacc      720
82   acctgacgct gaattgtact ggatctaaga atgtagtaaa ggttgtcatg atggtagagg      780
83   aatgcacgtg tgaagctcat aagagcaact tccaccaaac tgcacagttt aacatggata      840
84   catctactac cctgcaccat taaaggactg ccatacagta tggaaatgcc ctttttgttgg      900
85   aatatttgtt acatactatg catctaaagc attatgttgc cttctatttc atataaccac      960
86   atggaataag gattgtatga attataatta acaaatggca ttttgtgtaa catgcaagat     1020
87   ctctgttcca tcagttgcaa gataaaaggc aatatttgtt tgactttttt tctacaaaat     1080
88   gaatacccaa atatatgata agataatggg gtcaaaactg ttaaggggta atgtaataat     1140
89   agggactaag tttgcccagg agcagtgacc cataacaacc aatcagcagg tatgatttac     1200
90   tggtcacctg tttaaaagca aacatcttat tggttgctat gggttactgc ttctgggcaa     1260
91   aatgtgtgcc tcataggggg gttagtgtgt tgtgtactga ataaattgta tttatttcat     1320
92   tgttacaaaa aaaaaaaa                                                    1338
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95   <211> LENGTH: 318
96   <212> TYPE: PRT
97   <213> ORGANISM: Xenopus frazzled
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103                  20                 25                 30
104  Pro Val Arg Ile Pro Met Cys Lys Ser Met Pro Trp Asn Met Thr Lys
105              35                 40                 45
106  Met Pro Asn His Leu His His Ser Thr Gln Ala Asn Ala Ile Leu Ala
107          50                 55                 60
108  Ile Glu Gln Phe Glu Gly Leu Leu Thr Thr Glu Cys Ser Gln Asp Leu
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```
                            70                  75                  80
109  65
110  Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys Thr Ile Asp Phe
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112  Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys Glu Arg Ala Arg
113                  100                     105                 110
114  Ala Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His Thr Trp Pro Glu
115              115                     120                 125
116  Ser Leu Ala Cys Glu Glu Leu Pro Val Tyr Asp Arg Gly Val Cys Ile
117          130                     135                 140
118  Ser Pro Glu Ala Ile Val Thr Val Glu Gln Gly Thr Asp Ser Met Pro
119  145                 150                     155                 160
120  Asp Phe Ser Met Asp Ser Asn Asn Gly Asn Cys Gly Ser Gly Arg Glu
121                  165                     170                 175
122  His Cys Lys Cys Lys Pro Met Lys Ala Thr Gln Lys Thr Tyr Leu Lys
123                  180                     185                 190
124  Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Val Lys Val
125              195                     200                 205
126  Lys Cys His Asp Ala Thr Ala Ile Val Glu Val Lys Glu Ile Leu Lys
127          210                     215                 220
128  Ser Ser Leu Val Asn Ile Pro Lys Asp Thr Val Thr Leu Tyr Thr Asn
129  225                 230                     235                 240
130  Ser Gly Cys Leu Cys Pro Gln Leu Val Ala Asn Glu Glu Tyr Ile Ile
131                  245                     250                 255
132  Met Gly Tyr Glu Asp Lys Glu Arg Thr Arg Leu Leu Leu Val Glu Gly
133              260                     265                 270
134  Ser Leu Ala Glu Lys Trp Arg Asp Arg Leu Ala Lys Lys Val Lys Arg
135          275                     280                 285
136  Trp Asp Gln Lys Leu Arg Arg Pro Arg Lys Ser Lys Asp Pro Val Ala
137      290                     295                 300
138  Pro Ile Pro Asn Lys Asn Ser Asn Ser Arg Gln Ala Arg Ser
139  305                 310                     315
141  <210> SEQ ID NO: 4
142  <211> LENGTH: 1875
143  <212> TYPE: DNA
144  <213> ORGANISM: Xenopus frazzled
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149  ctaattctgc acttttaaat tatctgagta attgttcatt ttgtattgga tgggactaaa   180
150  gataaactta actccttgct tttgacttgc ccataaacta taaggtgggg tgagttgtag   240
151  ttgctttttac atgtgcccag attttccctg tattccctgt attccctcta aagtaagcct   300
152  acacatacag gttgggcaga ataacaatgt ctcgaacaag gaaagtggac tcattactgc   360
153  tactggccat acctggactg gcgcttctct tattacccaa tgcttactgt gcttcgtgtg   420
154  agcctgtgcg gatccccatg tgcaaatcta tgccatggaa catgaccaag atgcccaacc   480
155  atctccacca cagcactcaa gccaatgcca tcctggcaat tgaacagttt gaaggtttgc   540
156  tgaccactga atgtagccag gacctttgt tctttctgtg tgccatgtat gcccccattt   600
157  gtaccatcga tttccagcat gaaccaatta agccttgcaa gtccgtgtgc gaaagggcca   660
158  gggccggctg tgagcccatt ctcataaagt accggcacac ttggccagag agcctggcat   720
159  gtgaagagct gcccgtatat gacagaggag tctgcatctc cccagaggct atcgtcacag   780
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160  tggaacaagg aacagattca atgccagact tctccatgga ttcaaacaat ggaaattgcg    840
161  gaagcggcag ggagcactgt aaatgcaagc ccatgaaggc aacccaaaag acgtatctca    900
162  agaataatta caattatgta atcagagcaa aagtgaaaga ggtgaaagtg aaatgccacg    960
163  acgcaacagc aattgtggaa gtaaaggaga ttctcaagtc ttccctagtg aacattccta   1020
164  aagacacagt gacactgtac accaactcag gctgcttgtg cccccagctt gttgccaatg   1080
165  aggaatacat aattatgggc tatgaagaca aagagcgtac caggcttcta ctagtggaag   1140
166  gatccttggc cgaaaaatgg agagatcgtc ttgctaagaa agtcaagcgc tgggatcaaa   1200
167  agcttcgacg tcccaggaaa agcaaagacc ccgtggctcc aattcccaac aaaaacagca   1260
168  attccagaca agcgcgtagt tagactaacg gaaaggtgta tggaaactct atggactttg   1320
169  aaactaagat ttgcattgtt ggaagagcaa aaaagaaatt gcactacagc acgttatatt   1380
170  ctattgttta ctacaagaag ctggtttagt tgattgtagt tctcctttcc ttctttttttt   1440
171  ttataactat atttgcacgt gttcccaggc aattgtttta ttcaacttcc agtgacagag   1500
172  cagtgactga atgtctcagc ctaaagaagc tcaattcatt tctgatcaac taatggtgac   1560
173  aagtgtttga tacttgggga aagtgaacta attgcaatgg taaatcagag aaaagttgac   1620
174  caatgttgct tttcctgtag atgaacaagt gagagatcac atttaaatga tgatcacttt   1680
175  ccatttaata ctttcagcag ttttagttag atgacatgta ggatgcacct aaatctaaat   1740
176  attttatcat aaatgaagag ctggtttaga ctgtatggtc actgttggga aggtaaatgc   1800
177  ctactttgtc aattctgttt taaaaattgc ctaaataaat attaagtcct aaataaaaaa   1860
178  aaaaaaaaaa aaaaa                                                     1875
180  <210> SEQ ID NO: 5
181  <211> LENGTH: 896
182  <212> TYPE: PRT
183  <213> ORGANISM: Xenopus
185  <400> SEQUENCE: 5
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189           20                  25                  30
190  Glu Pro Pro Gly Thr Val Ile Ala Val Leu Ser Gln His Ser Ile Phe
191       35                  40                  45
192  Asn Thr Thr Asp Ile Pro Ala Thr Asn Phe Arg Leu Met Lys Gln Phe
193      50                  55                  60
194  Asn Asn Ser Leu Ile Gly Val Arg Glu Ser Asp Gly Gln Leu Ser Ile
195  65                  70                  75                  80
196  Met Glu Arg Ile Asp Arg Glu Gln Ile Cys Arg Gln Ser Leu His Cys
197                      85                  90                  95
198  Asn Leu Ala Leu Asp Val Val Ser Phe Ser Lys Gly His Phe Lys Leu
199                  100                 105                 110
200  Leu Asn Val Lys Val Glu Val Arg Asp Ile Asn Asp His Ser Pro His
201              115                 120                 125
202  Phe Pro Ser Glu Ile Met His Val Glu Val Ser Glu Ser Ser Ser Val
203          130                 135                 140
204  Gly Thr Arg Ile Pro Leu Glu Ile Ala Ile Asp Glu Asp Val Gly Ser
205  145                 150                 155                 160
206  Asn Ser Ile Gln Asn Phe Gln Ile Ser Asn Asn Ser His Phe Ser Ile
207                  165                 170                 175
208  Asp Val Leu Thr Arg Ala Asp Gly Val Lys Tyr Ala Asp Leu Val Leu
209              180                 185                 190
210  Met Arg Glu Leu Asp Arg Glu Ile Gln Pro Thr Tyr Ile Met Glu Leu
```

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                          195                        200                        205
211                                      Val Pro Ser Leu Ser Gly Thr Ala Val Val
212  Leu Ala Met Asp Gly Gly
213      210                      215
214  Asn Ile Arg Val Leu Asp Phe Asn Asp Asn Ser Pro Val Phe Glu Arg
215  225                      230                        235                        240
216  Ser Thr Ile Ala Val Asp Leu Val Glu Asp Ala Pro Leu Gly Tyr Leu
217                      245                        250                        255
218  Leu Leu Glu Leu His Ala Thr Asp Asp Asp Glu Gly Val Asn Gly Glu
219          260                          265                        270
220  Ile Val Tyr Gly Phe Ser Thr Leu Ala Ser Gln Glu Val Arg Gln Leu
221          275                      280                        285
222  Phe Lys Ile Asn Ser Arg Thr Gly Ser Val Thr Leu Glu Gly Gln Val
223          290                      295                        300
224  Asp Phe Glu Thr Lys Gln Thr Tyr Glu Phe Glu Val Gln Ala Gln Asp
225  305                      310                        315                        320
226  Leu Gly Pro Asn Pro Leu Thr Ala Thr Cys Lys Val Thr Val His Ile
227                      325                        330                        335
228  Leu Asp Val Asn Asp Asn Thr Pro Ala Ile Thr Ile Thr Pro Leu Thr
229          340                          345                        350
230  Thr Val Asn Ala Gly Val Ala Tyr Ile Pro Glu Thr Ala Thr Lys Glu
231          355                      360                        365
232  Asn Phe Ile Ala Leu Ile Ser Thr Thr Asp Arg Ala Ser Gly Ser Asn
233          370                      375                        380
234  Gly Gln Val Arg Cys Thr Leu Tyr Gly His Glu His Phe Lys Leu Gln
235  385                      390                        395                        400
236  Gln Ala Tyr Glu Asp Ser Tyr Met Ile Val Thr Thr Ser Thr Leu Asp
237                      405                        410                        415
238  Arg Glu Asn Ile Ala Ala Tyr Ser Leu Thr Val Val Ala Glu Asp Leu
239          420                      425                        430
240  Gly Phe Pro Ser Leu Lys Thr Lys Lys Tyr Tyr Thr Val Lys Val Ser
241      435                      440                        445
242  Asp Glu Asn Asp Asn Ala Pro Val Phe Ser Lys Pro Gln Tyr Glu Ala
243      450                      455                        460
244  Ser Ile Leu Glu Asn Asn Ala Pro Gly Ser Tyr Ile Thr Thr Val Ile
245  465                      470                        475                        480
246  Ala Arg Asp Ser Asp Ser Asp Gln Asn Gly Lys Val Asn Tyr Arg Leu
247                      485                        490                        495
248  Val Asp Ala Lys Val Met Gly Gln Ser Leu Thr Thr Phe Val Ser Leu
249          500                      505                        510
250  Asp Ala Asp Ser Gly Val Leu Arg Ala Val Arg Ser Leu Asp Tyr Glu
251          515                      520                        525
252  Lys Leu Lys Gln Leu Asp Phe Glu Ile Glu Ala Ala Asp Asn Gly Ile
253          530                      535                        540
254  Pro Gln Leu Ser Thr Arg Val Gln Leu Asn Leu Arg Ile Val Asp Gln
255  545                      550                        555                        560
256  Asn Asp Asn Cys Pro Val Ile Thr Asn Pro Leu Leu Asn Asn Gly Ser
257                      565                        570                        575
258  Gly Glu Val Leu Leu Pro Ile Ser Ala Pro Gln Asn Tyr Leu Val Phe
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VERIFICATION SUMMARY   DATE: 03/18/2002
PATENT APPLICATION: US/09/903,323A   TIME: 15:36:33

Input Set : A:\510015-261.TXT
Output Set: N:\CRF3\03182002\I903323A.raw